

[illegible]

(1)

(j)

~~(i)~~

(iii)

(iv)

(B) STREET: 6 BECKER FARM ROAD

(D) STATE: NEW JERSEY

(F) ZIP: 07068

(v)

(B) ~~COMPUTER~~: IBM PS/2

(D) ~~SOFTWARE~~: WORD PERFECT 5.1

(vi)

(B) ~~F~~ILING DATE: concurrently

ATTORNEY/AGENT INFORMATION:

(vii)

(C) REFERENCE/DOCKET NUMBER: 325800-

(viii)

(B) TELFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 666 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGAAGGT GTAGAATAAG TGGGAGGCC CCGGCGCCCC CCGGTGTCCC CGCCCAGGCC 60
CCTGTCTCCC AGCCTGATGC CCCTGGCCAC CAGAGGAAAG TGGTGTTCATG GATAGATGTG 120
TATACTCGCG CTACCTGCCA GCCCCGGGAG GTGGTGGTGC CCTTGACTGT GGAGCTCATG 180
GGCACC GTG CCAAACAGCT GGTGCCCAGC TGCCTGACTG TGCAGCGCTG TGGTGGCTGC 240
TGCCCTGACG ATGGCCTGGA GTGTGTGCCC ACTGGGCAGC ACCAAGTCCG GATGCAGATC 300
CTCATGATCC GGTACCCGAG CAGTCAGCTG GGGGAGATGT CCCTGGAAGA ACACAGCCAG 360
TGTGAATGCA GACCTAAAAA AAAGGACAGT GCTGTGAAGC CAGACAGGGC TGCTACTCCC 420
CACCACCGTC CCCAGCCCCG TTCTGTTC CGCTGGGACT CTGCCCCCGG AGCACCCCTCC 480
CCAGCTGACA TCACCCATC CCACTCCAGC CCCAGGCCCC TCTGCCCACG CTGCACCCAG 540
CACCACCACT GCCCTGACCC CCGGACCTGC CGCTGCCGCT GTCGACGCCG CAGCTTCCTC 600
CGTTGTCAAG GGCGGGGCTT AGAGCTCAAC CCAGACACCT GCAGGTGCCG GAAGCTGCGA 660
AGGTGA 666

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 221 AMINO ACIDS
(B) TYPE: AMINO ACID
(C) STRANDEDNESS:
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Arg Cys Arg Ile Ser Gly Arg Pro Pro Ala Pro Pro Gly
5 10 15
Val Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
20 25 30
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr
35 40 45
Cys Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met
50 55 60
Gly Thr Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln
65 70 75
Arg Cys Gly Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro
80 85 90
Thr Gly Gln His Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr
95 100 105
Pro Ser Ser Gln Leu Gly Glu Met Ser Leu Glu Glu His Ser Gln
110 115 120
Cys Glu Cys Arg Pro Lys Lys Lys Asp Ser Ala Val Lys Pro Asp
125 130 135
Arg Ala Ala Thr Pro His His Arg Pro Gln Pro Arg Ser Val Pro
140 145 150
Gly Trp Asp Ser Ala Pro Gly Ala Pro Ser Pro Ala Asp Ile Thr
155 160 165
Gln Ser His Ser Ser Pro Arg Pro Leu Cys Pro Arg Cys Thr Gln
170 175 180
His His Gln Cys Pro Asp Pro Arg Thr Cys Arg Cys Arg Cys Arg
185 190 195
Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu Asn
200 205 210
Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
215 220